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**RAW SEQUENCE LISTING
PATENT APPLICATION US/08/373,857**DATE: 06/08/95
TIME: 10:52:19**INPUT SET: S4067.raw**

This Raw Listing contains the General
Information Section and up to the first 5 pages.

HJ

SEQUENCE LISTING**1 (1) General Information:****2 (i) APPLICANT: Lobb, Roy R.****3 (ii) TITLE OF INVENTION: Treatment For Inflammatory Bowel Disease****4 (iii) NUMBER OF SEQUENCES: 4****5 (iv) CORRESPONDENCE ADDRESS:****6 (A) ADDRESSEE: LAHIVE & COCKFIELD****7 (B) STREET: 60 State Street, Suite 510****8 (C) CITY: Boston****9 (D) STATE: Massachusetts****10 (E) COUNTRY: USA****11 (F) ZIP: 02109-1875****12 (v) COMPUTER READABLE FORM:****13 (A) MEDIUM TYPE: Floppy disk****14 (B) COMPUTER: IBM PC compatible****15 (C) OPERATING SYSTEM: PC-DOS/MS-DOS****16 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25****17 (vi) CURRENT APPLICATION DATA:****18 (A) APPLICATION NUMBER: US 08/373,857****19 (B) FILING DATE: 18-JAN-1995****20 (C) CLASSIFICATION:****21 (vii) PRIOR APPLICATION DATA:****22 (A) APPLICATION NUMBER: US 08/284,603****23 (B) FILING DATE: 11-AUG-1994****24 (C) CLASSIFICATION:****25 (vii) PRIOR APPLICATION DATA:****26 (A) APPLICATION NUMBER: US 07/835,139****27 (B) FILING DATE: 12-FEB-1992****28 (C) CLASSIFICATION:****29 (vii) PRIOR APPLICATION DATA:****30 (A) APPLICATION NUMBER: PCT/US93/00924****31 (B) FILING DATE: 02-FEB-1993****32 (viii) ATTORNEY/AGENT INFORMATION:****33 (A) NAME: Louis Myers (PLM)****34 (B) REGISTRATION NUMBER: 35,965****ENTERED**

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47 (C) REFERENCE/DOCKET NUMBER: BGP-031USCP
48
49 (ix) TELECOMMUNICATION INFORMATION:
50 (A) TELEPHONE: (617)227-7400
51 (B) TELEFAX: (617)227-5941
52
53
54 (2) INFORMATION FOR SEQ ID NO:1:
55
56 (i) SEQUENCE CHARACTERISTICS:
57 (A) LENGTH: 360 base pairs
58 (B) TYPE: nucleic acid
59 (C) STRANDEDNESS: single
60 (D) TOPOLOGY: linear
61
62 (ii) MOLECULE TYPE: cDNA
63
64
65 (ix) FEATURE:
66 (A) NAME/KEY: CDS
67 (B) LOCATION: 1..360
68
69 (ix) FEATURE:
70 (A) NAME/KEY: misc_feature
71 (B) LOCATION: 1
72 (D) OTHER INFORMATION: /note= "pBAG159 insert:
73 HP1/2 heavy vchain variable region; amino acid 1 is
74 Glu (E) but Gln (Q) may be substituted"
75
76
77 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
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79 GTC AAA CTG CAG CAG TCT GGG GCA GAG CTT GTG AAG CCA GGG GCC TCA 48
80 Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
81 1 5 10 15
82
83 GTC AAG TTG TCC TGC ACA GCT TCT GGC TTC AAC ATT AAA GAC ACC TAT 96
84 Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
85 20 25 30
86
87 ATG CAC TGG GTG AAG CAG AGG CCT GAA CAG GGC CTG GAG TGG ATT GGA 144
88 Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
89 35 40 45
90
91 AGG ATT GAT CCT GCG AGT GGC GAT ACT AAA TAT GAC CCG AAG TTC CAG 192
92 Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
93 50 55 60
94
95 GTC AAG GCC ACT ATT ACA GCG GAC ACG TCC TCC AAC ACA GCC TGG CTG 240
96 Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
97 65 70 75 80
98
99 CAG CTC AGC AGC CTG ACA TCT GAG GAC ACT GCC GTC TAC TAC TGT GCA 288

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100 Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
101 85 90 95
102
103 GAC GGA ATG TGG GTA TCA ACG GGA TAT GCT CTG GAC TTC TGG GGC CAA 336
104 Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
105 100 105 110
106
107 GGG ACC ACG GTC ACC GTC TCC TCA 360
108 Gly Thr Thr Val Thr Val Ser Ser
109 115 120
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112 (2) INFORMATION FOR SEQ ID NO:2:
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114 (i) SEQUENCE CHARACTERISTICS:
115 (A) LENGTH: 120 amino acids
116 (B) TYPE: amino acid
117 (D) TOPOLOGY: linear
118
119 (ii) MOLECULE TYPE: protein
120
121 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
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123 Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
124 1 5 10 15
125
126 Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
127 20 25 30
128
129 Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
130 35 40 45
131
132 Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
133 50 55 60
134
135 Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
136 65 70 75 80
137
138 Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
139 85 90 95
140
141 Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
142 100 105 110
143
144 Gly Thr Thr Val Thr Val Ser Ser
145 115 120
146
147 (2) INFORMATION FOR SEQ ID NO:3:
148
149 (i) SEQUENCE CHARACTERISTICS:
150 (A) LENGTH: 318 base pairs
151 (B) TYPE: nucleic acid
152 (C) STRANDEDNESS: single

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153      (D) TOPOLOGY: linear
154
155      (ii) MOLECULE TYPE: cDNA
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157
158      (ix) FEATURE:
159          (A) NAME/KEY: CDS
160          (B) LOCATION: 1..318
161          (D) OTHER INFORMATION: /product= "HP1/2 light
162              chain variable region"
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164      (ix) FEATURE:
165          (A) NAME/KEY: misc_feature
166          (B) LOCATION: 1
167          (D) OTHER INFORMATION: /note= "pBAG172 insert:
168              HP1/2 light chain variable region"
169
170
171      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
172

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173 AGT ATT GTG ATG ACC CAG ACT CCC AAA TTC CTG CTT GTT TCA GCA GGA	48
174 Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly	
175 1 5 10 15	
176	
177 GAC AGG GTT ACC ATA ACC TGC AAG GCC AGT CAG AGT GTG ACT AAT GAT	96
178 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp	
179 20 25 30	
180	
181 GTA GCT TGG TAC CAA CAG AAG CCA GGG CAG TCT CCT AAA CTG CTG ATA	144
182 Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile	
183 35 40 45	
184	
185 TAT TAT GCA TCC AAT CGC TAC ACT GGA GTC CCT GAT CGC TTC ACT GGC	192
186 Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly	
187 50 55 60	
188	
189 AGT GGA TAT GGG ACG GAT TTC ACT TTC ACC ATC AGC ACT GTG CAG GCT	240
190 Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala	
191 65 70 75 80	
192	
193 GAA GAC CTG GCA GTT TAT TTC TGT CAG CAG GAT TAT AGC TCT CCG TAC	288
194 Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr	
195 85 90 95	
196	
197 ACG TTC GGA GGG GGG ACC AAG CTG GAG ATC	318
198 Thr Phe Gly Gly Thr Lys Leu Glu Ile	
199 100 105	
200	
201	
202 (2) INFORMATION FOR SEQ ID NO:4:	
203	
204 (i) SEQUENCE CHARACTERISTICS:	
205 (A) LENGTH: 106 amino acids	

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206 (B) TYPE: amino acid
207 (D) TOPOLOGY: linear
208
209 (ii) MOLECULE TYPE: protein
210
211 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
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214 1 5 10 15
215
216 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp
217 20 25 30
218
219 Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
220 35 40 45
221
222 Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
223 50 55 60
224
225 Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
226 65 70 75 80
227
228 Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
229 85 90 95
230
231 Thr Phe Gly Gly Thr Lys Leu Glu Ile
232 100 105
233
234
235

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SEQUENCE VERIFICATION REPORT
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